



SEQUENCE LISTING

<110> GONG, Zhiyuan
LAM, Toong Jin
JU, Bensheng
XU, Yanfei
HE, Jiangyan
YAN, Tie

<120> CHIMERIC GENE CONSTRUCTS FOR GENERATION OF
FLUORESCENT TRANSGENIC ORNAMENTAL FISH

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<140> 10/605,708

<141> 2003-10-22

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ctg tcc ctg cgg ggc aag gcc gtc gtg ctc atg ggg aaa aac acc atg 254
Leu Ser Leu Arg Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met
45 50 55 60
atg agg aag gcc att cgt ggc cac ctg gaa aac aac cca gct ctg gag 302
Met Arg Lys Ala Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu
65 70 75
agg ctg ctt ccc cac atc cgc ggg aac gtg ggc ttc gtc ttc acc aag 350
Arg Leu Leu Pro His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys
80 85 90
gag gat ctg act gag gtc cga gac ctg ctg ctg gca aac aaa gtg ccc 398
Glu Asp Leu Thr Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro
95 100 105
gct gct gcc cgt gct ggt gcc atc gcc ccc tgt gag gtg act gtg ccg 446
Ala Ala Ala Arg Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro
110 115 120
gcc cag aac acc ggg ctc ggt cct gag aag acc tct ttc ttc cag gct 494
Ala Gln Asn Thr Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala
125 130 135 140
ttg gga atc acc acc aag atc tcc aga gga acc att gaa atc ttg agt 542
Leu Gly Ile Thr Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser
145 150 155
gac gtt cag ctt atc aaa cct gga gac aag gtg ggc gcc agc gag gcc 590
Asp Val Gln Leu Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala
160 165 170
acg ctg ctg aac atg ctg aac atg ctg aac atc tcg ccc ttc tcc tac 638
Thr Leu Leu Asn Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr

175	180	185	
ggg ctg atc atc cag cag gtg tat gat aac ggc agt gtc tac agc ccc			686
Gly Leu Ile Ile Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro			
190	195	200	
gag gtg ctg gac atc act gag gac gcc ctg cac aag agg ttc ctg aag			734
Glu Val Leu Asp Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys			
205	210	215	220
ggg gtg agg aac atc gcc agt gtg tgt ctg cag atc ggc tac cca act			782
Gly Val Arg Asn Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr			
225	230	235	
ctt gct tcc atc cct cac act atc atc aat gga tac aag agg gtc ctg			830
Leu Ala Ser Ile Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu			
240	245	250	
gct gtc act gtc gaa aca gac tac aca ttc ccc ttg gct gag aag gtg			878
Ala Val Thr Val Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val			
255	260	265	
aag gcc tac ctg gct gat ccc acc gct ttc gct gtt gca gcc cct gtt			926
Lys Ala Tyr Leu Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val			
270	275	280	
gcg gca gct aca gag cag aaa tcc gct gct cct gcg gct aaa gag gag			974
Ala Ala Ala Thr Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu			
285	290	295	300
gca ccc aag gag gat tct gag gag tct gat gaa gac atg ggc ttc ggc			1022
Ala Pro Lys Glu Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly			
305	310	315	
ctg ttt gat taa accagacacc gaatatccat gtctgttttaa catcaataaa			1074
Leu Phe Asp			
320			
acatctggaa aaaaaaaaaa aaaaaaaaaa			1104

<210> 6

<211> 319

<212> PRT

<213> Danio rerio

<400> 2

Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn Tyr Phe Leu Lys			
1	5	10	15
Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe Ile Val Gly Ala			
20	25	30	
Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg Leu Ser Leu Arg			
35	40	45	
Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met Arg Lys Ala			
50	55	60	
Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Arg Leu Leu Pro			
65	70	75	80

His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu Asp Leu Thr
 85 90 95
 Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro Ala Ala Ala Arg
 100 105 110
 Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala Gln Asn Thr
 115 120 125
 Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu Gly Ile Thr
 130 135 140
 Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp Val Gln Leu
 145 150 155 160
 Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala Thr Leu Leu Asn
 165 170 175
 Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr Gly Leu Ile Ile
 180 185 190
 Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro Glu Val Leu Asp
 195 200 205
 Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys Gly Val Arg Asn
 210 215 220
 Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr Leu Ala Ser Ile
 225 230 235 240
 Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Val Thr Val
 245 250 255
 Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val Lys Ala Tyr Leu
 260 265 270
 Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val Ala Ala Ala Thr
 275 280 285
 Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu Ala Pro Lys Glu
 290 295 300
 Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu Phe Asp
 305 310 315

<210> 7
 <211> 2241
 <212> DNA
 <213> Danio rerio

<220>
 <221> TATA signal
 <222> (2103)..(2108)

<220>
 <221> primer bind
 <222> (2221)_(2241)
 <223> CK2

<220>
 <221> misc feature
 <222> (2142)..(2235)
 <223> Identical to the 5' CK cDNA

<400> 7
 ccttcccttc tactttttgac gtccttttta gattactcat ctcaaacacc catacaaagg 60
 tcacacctgg tttatactat gatagttgta cagtgtggtg tgtgacaccc aactgtgtgcc 120
 aattgtctga ctatgcaggg tgtctatgct tatagtttac agttagacca aagtgtgtctg 180
 gtgtgtgaag taacaaatga caaatactca aattgtaatt tactaagtag tttaaaaatg 240
 tagtgcagtg ttggtacttt tatttcactt ttattcctgt ctatgtggat tagacaaatc 300

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acatagaagg taaatcacat cataatgaac agcaaaactgt ttgccagcat taaaagaaga 360
agactgctta gatgcatgtc actgatgaga aaataacttt aaacgcacac aagacggcac 420
gtacccaac gcagtgggga cgttgcattht gaactcaacg tcaggtcgat gtcaatgttc 480
ctaattgatgt tacagcttga tgttatgcgg ggattatggg tgccatacct gatgaataaa 540
ggttcgacat tggatttttg tcgctttcca cctatgacat cgttatttga cgtcaaaata 600
aatttaggtc accacaacct atatttaacc tgctgggcaa taactaaatg cactacagaa 660
taaatgcatc agctttttcac agcataatac aaaagctact tttcactcat actttgagta 720
acatttttag gcatgtattg atatttttac cagccctccc catacataat cgtatgttta 780
acattagctt tgtagccgc tagcattact gagcttggtc atgaaagcag atttgagct 840
gatgattgcc gtaccatgat ctcacacctt gacgattgcg taatgctatt aaatgcccc 900
atttcgtgtt gacttgcacg agaaatgaga tgggaacatt tatcagtggg cattaaatac 960
tatttttgtg tttagcttagc tgcagttttt aactattgta attaaagtagt ttttctcaga 1020
tgtactttta ctttcccttg agtacatttt ccttccttca acctgcagtc actactttat 1080
agtccgtgta ttccctgtcca atcaaattgc taccttaaga catgggccat ttataattgc 1140
tgtcaaaaat atttacacgc attaacccag agatgatgga tgtttactgt atgatgaccg 1200
aagacgtcaa catggcggtta ggttgacgtt tgttttagaaa tgaaaattag gttgacgtca 1260
aacatccaat ctaaaatcat atatcaatgt atgttaccct tatgacgtct atcagacgtt 1320
tgtcattatt tgacgttggg ttaagatgtt acacaacct aatccaccaa atattaactt 1380
acaatatcct tagatgctgg ctagactttg taatattaac atcttatgat gttgtgtgcc 1440
tgttacgttt acacacatgt aaattacatg tctactacta ctactcttga gtacttttaa 1500
atattttcaa ctgatacttt tactcgcact tatgattttt cagtactctt tccactactg 1560
cacatatggt ggagtttaga gccataatct gtgcagaatt gtgtgtgtgc acattttcca 1620
atatcaatac agaaggaaaac tgtgttccct gttcccttgt aaatctcaac aatgcaactg 1680
ttcagctcag ggggaaaaat gccctgccag atccaaacgg ctggcaaaaag tgaatggaaa 1740
aaagcctttc attaatgtga aagttgctgc gcgccccacc cagataaaaa gagcagaggt 1800
taacatgctc tctacggctg tccagccaac cagatactga ggcagaaaca caccgctgg 1860
cagatgggtga gagctacact gtcttttcca gagtttctac tggaatgcct gtcctcaagt 1920
ctcaagctc tccttgcatc ctctcattcc acctggggca aagccccagg ctgggtgtga 1980
caacatttat cttaccactt tctctctgta cctgtctaac aggtagggtg tgtgtgagag 2040
tgcgtatgtg tgcaagtgcg tgtgtgtgtg agagcagtca gctccaccct ctcaagagtg 2100
tgtataaaat tggtcagcca gctgctgaga gacacgcaga gggactttga ctctcctttg 2160
tgagcaacct cctccactca ctctctctc agagagcact ctctgtacct cttctcagca 2220
actcaaagac acaggatccg g                                     2241

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```

<210> 8
<211> 1456
<212> DNA
<213> Danio rerio

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<220>
<221> TATA signal
<222> (1389)..(1394)

```

```

<220>
<221> primer bind
<222> (1433)_(1456)
<223> MCK2

```

```

<220>
<221> misc feature
<222> (1428)..(1453)
<223> Identical to the 5' MCK cDNA

```

```

<400> 8
gaattgcaaa gtcagagtaa taaaatgaaa ccaaaaaaca tttttaaata tacttgtctc 60
tgtgggcttaa tcttggctga tgtgtgtgtg tgtgtgtgtg tacttgacag ctgctagtga 120
gcatgtgcac catgacaggc ctgttattca cacttggtgc catgttggag actgttcggc 180

```

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cagctatagt tttcttcaca gagtcctggg tcacctaattg tcacaaggaa gaaacatggt 240
acatgttaaa atgtgacatt caaattgtag tgcattactt aacgaaacgc attacacaag 300
ttacagctta aaagattgct agacagaaaa accagggagg ggttttccca taatatccag 360
tgagactcta ggagcgggaa cactaacagg cctccctgag tgagaacatt gcatgtgcgc 420
gtgacagaaa accagagatg gaaatacctt cttttgaatt gcataattgc ttaaaagaag 480
acacaacagg gatagttcac ccaaaaaaca gaccattctt tttttctggt gaacaaaaat 540
taagatattt tgaagaatgc ttaccgaata acttccatat ttggaaacta attacagtga 600
aagtcaatgg gtcttccagc attttttcaa tataccttac tttgagttca aaagaaaaaac 660
acatctcaaa taggtttgag gttgaataaa catttttcat tttgggggtgg actatcccta 720
attatttgac acttaagatt tatagtaaatt cattttatag actttctccc cttattaaac 780
atggttgaat ttatcttcat gtttatgtct gggttgtgct tttttgaaaa gatttccttg 840
tcaaatgttt ttgtgtatgg ttggcgcaca atagactgaa ctggcctatc acacagactt 900
tcataacaac tccagttgat gccctttcac cctcagtgtg taaatatggc gtctgacatg 960
agcagattaa acacgacact gcaacaactt tacctgtaaa aatacaaat gagtttgcac 1020
ccagaatcat gtggtgaacg aagcctacca agagattttt gaaagccatc ggcctgacac 1080
gcgcacttct gatatctgtg gtatgtttgg caaaagtgtc gctcagcctt tttagcatgg 1140
cagatcctcc acatcccac acccctcctt caacctattc cctcctggaa agctatgtat 1200
ggggcgggaa gtgtaaatgg atatgggaag gaaggggggc accaccaca gctgccacct 1260
catctaggat gcctggggcc taaattgaag cctttcttac actaaacagg gcataagaga 1320
ccagcgccag ccaatcataa ttcagtgaac tctaaaatgg gccagccaat ggctgcaggg 1380
gctagaggta tatatatcca aatcaaactc ttcttgcttg ggtgaccctt atttcggctt 1440
ggatgaacagg atccggg                                     1456

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```

<210> 9
<211> 2205
<212> DNA
<213> Danio rerio

```

```

<220>
<221> primer bind
<222> (2179)..(2205)
<223> ARP2

```

```

<220>
<221> misc_feature
<222> (2153)..(2199)
<223> Identical to the 5' ARP cDNA

```

```

<220>
<221> intron
<222> (792)..(2152)

```

```

<220>
<221> misc_feature
<222> (775)..(791)
<223> Identical to the 5' ARP cDNA

```

```

<400> 9
atctgtatta agaaacactt aaaatatata tgcgttacga attaaaaaca aaacacgatc 60
attttaattt gtgttgata attttacatt ttgtaagtat tatttttata aaaaatatat 120
agaaataata caaatttggt tacagtattc ttagttattg caataaacga attttatata 180
gaaagagaaa gagttttatt ataagatgtt caatttaaaa aatggcagaa aatagaaaaa 240
tgattgtcaa gatgataaaa gtcagttagt acaaaaaaat aagatgaaaa acatcaaaat 300
agataataaa gtgacttttt tgggcggacc aaatttcctt attaatgggt aattcattaa 360
aatacattca ttaaaataaa ggtattgcga tgaatttaga tgcacagtga ttttggttct 420
gtgcagattt ttggctgttg ttagaaggga tacatctgcg gccgaaagtt aacgggaact 480

```

```

atttacattc tttgctatta aattatccat tatttgattt ttattacccc aaccgtaaac 540
tcaaccctca cagtaatgta aaaatattat ttattgtttt atagcgtcac agaatgatgc 600
tatattgacc gcagctgtat cctttctaag tgcgactgta caaatacgca ctgaccgtga 660
cagacacgtg cattgaccaa tcagcgcaca gatacgcat ttcgcgcga ttctgattgg 720
atgatcgact gatactaata ttgtgccgct tcctttcgcg gcctccttct ttcacgcgtc 780
cctaccgtga ggtaaggctg acgccgctct tgtggcgggt tcttaaaaatg tgtaataaaa 840
taacatcata agaggtcacg agaaggctca cgtgtgttta atatcagcgg cggttattat 900
tatgcgttta aagcttgtgt aatgattttt acagtaaaag ttagcactag cctgttagca 960
caggcctcgt gcgccatgtg tgacgcgcacg ttttaatagc atcttatttg attttgatga 1020
tccgattctg atattaatca tatttatgcg taaaatgtgt gatgggtctg ctagtgga 1080
ttacatgcta gtacttgtgc tagtcggtcg atccacattg agatgttgcg ctatttgcca 1140
ttttaaaacc agttactctc atttttagtga aatattctta agccactaag ttaaaaattg 1200
tcaatcacat ataattgtgt ttatgtttta tttgagtcac cataccagg taaagtattt 1260
tttataattag tatgtacaat ttggcataaa ctgccttcgg ttttgattga catctacttt 1320
gtaaaggtaa tcttaaaagg gttaaaggctc acccaaaaga caattcaccc tcaagtgttt 1380
tcaaacttta tgagtttctt aatgaacatg gtatgttttg gagaaaactg gaaaccaact 1440
accataatac aaatacagga aaaatatact atagaagtcg atggttacag gttttctgca 1500
ttcaaaatat ctacacaagt gtttaatgga aggaactcaa gtgatttgaa aagttaagg 1560
tgcataaaatc agttttcatt tgggtgagct gtctctaaac atttgattta gacacctcag 1620
gcagtggta ccaagcttgt tcctgaaggg ccagtgctct acagatttta gctccaaccc 1680
taattaaaca cacctgaaca agctaataca ggtcttacta ggtatgtttg aaacatccag 1740
gcaggtgtgt tgatgcaaga tagagctaaa ccctgcaggg acaatggccc aacaggattg 1800
gtgacccctg cctcaagcca tcacaaatgc attatggtat taagaaatgt gcaggttcag 1860
ttatggacag gctgttgcag tgcttgttcg tcgttcccac tgcacaaatg aacatgattc 1920
cttctatccc tgtctgtctg catctcatga cttgcaggga cgctggtctc agacacgttt 1980
atagcagtaa atcaaataca atagtgtctc gattatcttt aaatatttga aagcttataa 2040
taggcaacca aattacctgg aaacagttta caaacagtaa ttcataattt gtcatttaat 2100
aagatgcaca caaggcagg gttaaagtat tgcttggtgt tgtaatcctc agattttaca 2160
accttgtctt taaaccggct gttcaccgat ccttgggaagg gatcc 2205

```

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cytokeratin - gene specific primer

<400> 10

cgctggagta agagatagac ctgg

24

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cytokeratin gene specific primer

<220>

<221> misc feature

<222> (1)..(6)

<223> Introduced for restriction site

<220>

<221> misc feature

<222> (3)..(8)

<223> BamHI site

<400> 11

ccggatcctg tgtctttgag ttgctg

26

<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Muscle creatine kinase gene specific primer

<220>

<221> misc feature

<222> (3)..(8)

<223> BamHI site

<400> 12

ccggatcctt gggatcagat cctg

24

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Muscle creatine kinase gene specific primer

<220>

<221> misc feature

<222> (1)..(3)

<223> Introduced for restriction site

<220>

<221> misc feature

<222> (3)..(B)

<223> BamHI site

<400> 13

ccggatcctg ttcaccaagc cgaa

24

<210> 14

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Acidic ribosomal protein PO gene specific primer

<400> 14
tagttggact tccacgtgcc ctgtc 25

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Acidic ribosomal protein PO gene specific primer

<220>
<221> misc feature
<222> (1)..(7)
<223> Introduced for restriction site

<220>
<221> misc feature
<222> (1)..(6)
<223> BamHI site

<400> 15
ggatcccttc caaggatcgg tgaaca 26

<210> 16
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated PCR

<400> 16
gttcattcttt acaagctagc gctgaacaat gctgtggaca agcttgaatt c 51

<210> 17
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated PCR

<220>
<223> n is a dideoxycytidine

<400> 17
gaattcaagn 10

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
linker specific primer

<400> 18
gttcacatcttt acaagctagc g 21

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
linker specific primer

<400> 19
tcctgaacaa tgctgtggac 20

<210> 20
<211> 1392
<212> DNA
<213> Danio rerio

<220>
<221> CDS
<222> (42)..(551)

<220>
<221> primer bind
<222> (6)..(28)
<223> M2

<220>
<221> primer bind
<222> (23)..(45)
<223> M1

<220>
<221> polyA signal
<222> (797)..(802)

<220>
<221> polyA_signal <222> (1351)..(1357)

<400> 20
ctcttcttga tcttctttaga cttcacacat accgtctcga c atg gca ccc aag aag 56
Met Ala Pro Lys Lys
1 5

gcc aag agg agg gca gca gga gga gag ggt tcc tcc aac gtc ttc tcc 104
Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser Ser Asn Val Phe Ser
10 15 20

atg ttt gag cag agc cag att cag gag tac aaa gag gct ttc aca atc 152
Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys Glu Ala Phe Thr Ile
25 30 35

att gac cag aac aga gac ggt atc atc agc aaa gac gac ctt agg gac 200
Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys Asp Asp Leu Arg Asp
40 45 50

gtg ttg gcc tca atg ggc cag ctg aat gtg aag aat gag gag ctg gag 248
Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys Asn Glu Glu Leu Glu
55 60 65

gcc atg atc aag gaa gcc agc ggc cca atc aac ttc acc gtt ttc ctc 296
Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn Phe Thr Val Phe Leu
70 75 80 85

acc atg ttc gga gag aag ttg aag ggt gct gac ccc gaa gac gtc atc 344
Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp Pro Glu Asp Val Ile
90 95 100

gtg tct gcc ttc aag gtg ctg gac cct gag ggc act gga tcc atc aag 392
Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly Thr Gly Ser Ile Lys
105 110 115

aag gaa ttc ctt gag gag ctt ttg acc act cag tgc gac agg ttc acc 440
Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln Cys Asp Arg Phe Thr
120 125 130

gca gag gag atg aag aat ctg tgg gcc gcc ttc ccc cca gat gtg gct 488
Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe Pro Pro Asp Val Ala
135 140 145

ggc aat gtt gac tac aag aac atc tgc tac gtc atc aca cac gga gag 536
Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val Ile Thr His Gly Glu
150 155 160 165

gag aag gag gag taa acaaccttgg aatagaggaa acgaagagaa gaacatgcat 591
Glu Lys Glu Glu
170

cctcacagct taatctccag tctgttgtct ggccttctct aactttttgtt tttccttcct 651

ccctttcttg ctttctacca tcgttggttac tccaagcact tacactctcc atcttaccaa 711

agacttgtct cgctgggact gaattgggag ggtggagagg aacacgacca cagtgtctgt 771

cgagtgggga catgggattg ttttcaataa aatgaacatc atttctgtat ctctcacatt 831

ctctctttct ctctgtttct cactcattac ccacaacccc tctctttcat ttcagtcaag 891

cttgcattga agtcgctgct tcttctgctg cagtcttagg agttgaaacg aaggcatcta 951

tagtttgggg ctgaaacatc tctctagatc aatgtggaag agtgctcact ctgaggggga 1011

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aagaagcacg atggagtgat ctcaactctat aatagaggaa ccagtcatca ttctcatttc 1071
ctcctctgggt ggttgactaa aaagagaaaag agaaaatgag ggttttgtgc tgagtgagtt 1131
tagcctccta aaagcgaatgc cgagctcatc acagagggag tgagagggac agaccatcct 1191
aggaagagag gagagcaggg actgaaagaa aacataacct cttcactccc cctctcccct 1251
cctcttctct atttctctgt ccactcttttc ttttttcttt tttctttttt gctttctgca 1311
tctgggcctg ctttgctctg ccaaacctct cctgtaacca ataaaaagac acaaactgtg 1371
aataaaaaaa aaaaaaaaaa a                                     1392

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<210> 21
<211> 169
<212> PRT
<213> Danio rerio

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```

<400> 21
Met Ala Pro Lys Lys Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser
 1          5          10          15
Ser Asn Val Phe Ser Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys
          20          25          30
Glu Ala Phe Thr Ile Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys
          35          40          45
Asp Asp Leu Arg Asp Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys
          50          55          60
Asn Glu Glu Leu Glu Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn
          65          70          75          80
Phe Thr Val Phe Leu Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp
          85          90          95
Pro Glu Asp Val Ile Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly
          100          105          110
Thr Gly Ser Ile Lys Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln
          115          120          125
Cys Asp Arg Phe Thr Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe
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Pro Pro Asp Val Ala Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val
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23